SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gregory Plowman
Douglas Clary

(ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF Alk-7 RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Filed herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/044,428
(B) FILING DATE: April 28, 1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 234/118

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 489-1600
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(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1793 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CGGCCACACT GACTAGAGCC AACCGCGCAC TTCAAAAGGG TGTCGGTGCC GCGCTCCCCT     60
CCCGCGGCCC GGGAACTTCA AAGCGGGCCG TGCTGCCCCG GCTGCCTCGC TCTGCTCTGG    120
GGCCTCGCAG CCCCGGCGCG GCCGCCTGGT GGCGATGACC CGGGCGCTCT GCTCAGCGCT    180
CCGCCAGGCT CTCCTGCTGC TCGCAGCGGC CGCCGAGCTC TCGCCAGGAC TGAAGTGTGT    240
ATGTCTTTTG TGTGATTCTT CAAACTTTAC CTGCCAAACA GAAGGAGCAT GTTGGGCATC    300
AGTCATGCTA ACCAATGGAA AAGAGCAGGT GATCAAATCC TGTGTCTCCC TTCCAGAACT    360
GAATGCTCAA GTCTTCTGTC ATAGTTCCAA CAATGTTACC AAAACCGAAT GCTGCTTCAC    420
AGATTTTTGC AACAACATAA CACTGCACCT TCCAACAGCA TCACCAAATG CCCCAAAACT    480
TGGACCCATG GAGCTGGCCA TCATTATTAC TGTGCCTGTT TGCCTCCTGT CCATAGCTGC    540
GATGCTGACA GTATGGGCAT GCCAGGGTCG ACAGTGCTCC TACAGGAAGA AAAAGAGACC    600
AAATGTGGAG GAACCACTCT CTGAGTGCAA TCTGGTAAAT GCTGGAAAAA CTCTGAAAGA    660
TCTGATTTAT GATGTGACCG CCTCTGGATC TGGCTCTGGT CTACCTCTGT TGGTTCAAAG    720
GACAATTGCA AGGACGATTG TGCTTCAGGA AATAGTAGGA AAAGGTAGAT TTGGTGAGGT    780
GTGGCATGGA AGATGGTGTG GGGAAGATGT GGCTGTGAAA ATATTCTCCT CCAGAGATGA    840
AAGATCTTGG TTTCGTGAGG CAGAAATTTA CCAGACGGTC ATGCTGCGAC ATGAAAACAT    900
CCTTGGTTTC ATTGCTGCTG ACAACAAAGA TAATGGAACT TGGACTCAAC TTTGGCTGGT    960
ATCTGAATAT CATGAACAGG GCTCCTTATA TGACTATTTG AATAGAAATA TAGTGACCGT   1020
GGCTGGAATG ATCAAGCTGG CGCTCTCAAT TGCTAGTGGT CTGGCACACC TTCATATGGA   1080
GATTGTTGGT ACACAAGGTA AACCTGCTAT TGCTCATCGA GACATAAAAT CAAAGAATAT   1140
CTTAGTGAAA AAGTGTGAAA CTTGTGCCAT AGCGGACTTA GGGTTGGCTG TGAAGCATGA   1200
TTCAATACTG AACACTATCG ACATACCTCA GAATCCTAAA GTGGGAACCA AGAGGTATAT   1260
GGCTCCTGAA ATGCTTGATG ATACAATGAA TGTGAATATC TTTGAGTCCT TCAAACGAGC   1320
TGACATCTAT TCTGTTGGTC TGGTTTACTG GGAAATAGCC CGGAGGTGTT CAGTCGGAGG   1380
AATTGTTGAG GAGTACCAAT TGCCTTATTA TGACATGGTG CCTTCAGATC CCTCGATAGA   1440
GGAAATGAGA AAGGTTGTTT GTGACCAGAA GTTTCGACCA AGTATCCCAA ACCAGTGGCA   1500
AAGTTGTGAA GCACTCCGAG TCATGGGGAG AATAATGCGT GAGTGTTGGT ATGCCAACGG   1560
AGCGGCCCGC CTAACTGCTC TTCGTATTAA GAAGACTATA TCTCAACTTT GTGTCAAAGA   1620
AGACTGCAAA GCCTAATGAT GATAATTATG TTAAAAAGAA ATCTCTCATA GCTTTCTTTT   1680
CCATTTTCCC CTTTATGTGA ATGTTTTTGC CATTTTTTTT TTGTTCTACC TCAAAGATAA   1740
GACAGTACAG TATTTAAGTG CCCATAAGGC AGCATGAAAA GATAACTCTA AAG          1793
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Thr Arg Ala Leu Cys Ser Ala Leu Arg Gln Ala Leu Leu Leu Leu
 1               5                  10                  15

Ala Ala Ala Ala Glu Leu Ser Pro Gly Leu Lys Cys Val Cys Leu Leu
            20                  25                  30
```

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala
35 40 45

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ile Lys Ser Cys Val
50 55 60

Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn
65 70 75 80

Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr
85 90 95

Leu His Leu Pro Thr Ala Ser Pro Asn Ala Pro Lys Leu Gly Pro Met
100 105 110

Glu Leu Ala Ile Ile Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala
115 120 125

Ala Met Leu Thr Val Trp Ala Cys Gln Gly Arg Gln Cys Ser Tyr Arg
130 135 140

Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu Ser Glu Cys Asn Leu
145 150 155 160

Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Val Thr Ala
165 170 175

Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala
180 185 190

Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu
195 200 205

Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe
210 215 220

Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln
225 230 235 240

Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp
245 250 255

Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr
260 265 270

His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr
275 280 285

Val Ala Gly Met Ile Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala
290 295 300

His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala
305 310 315 320

His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Glu Thr
325 330 335

Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Leu
340 345 350

Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr
355 360 365

```
Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu
    370                 375                 380

Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu
385                 390                 395                 400

Ile Ala Arg Arg Cys Ser Val Gly Gly Ile Val Glu Glu Tyr Gln Leu
                405                 410                 415

Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg
            420                 425                 430

Lys Val Val Cys Asp Gln Lys Phe Arg Pro Ser Ile Pro Asn Gln Trp
        435                 440                 445

Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys
    450                 455                 460

Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys
465                 470                 475                 480

Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
                485                 490
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 6 and 7 stand for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
His Arg Asp Leu Lys Xaa Xaa Asn
 1               5
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G. The letter "N" stands for Inosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GARRARGTNG CNGTNAARRT NTT 23

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "R" stands for A or G.
The letter "N" stands for Inosine.
The letter "K" stands for G or T.
The letter "M" stands for A or C.
The letter "Y" stands for C or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTRATRTCNC KRTGNGMNAT NGMNGGYTT 29

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 2 stands for Lys or Glu. "Xaa" in position 7 stands for Val or Ile.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Xaa Val Ala Val Lys Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 3 stands for Ala or Ser. "Xaa" in position 5 stands for Ala or Ser.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Lys Pro Xaa Ile Xaa His Arg Asp Ile Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AACTTTGGCT GGTATCTGAA TATC 24

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCTTGTGTAC CAACAATCTC CATA 24

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCCAGAGAT GAGAGATCTT GG 22

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TTCCAGCCAC GGTCACTATG TT 22

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Tyr Arg Lys Lys Lys Arg Pro Asn Val Glu Glu Pro Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTTCGAAAGC TTGAAATCGG TACCATCGAT TCTAGAGTTA ACTTCGAA 48

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCTAGAACG CGTTAAGGCG CGCCAATATC GATGAATTCT TCGAAGC 47